

Amendments to the Claims

Claim 1 (Original): An isolated polynucleotide encoding a protein having expansin activity wherein said polynucleotide hybridizes under high stringency conditions corresponding to 6X SSC, 50% formamide and 42°C, and washing at 0.2 X SSC at 65°C with the complement of the sequence set forth in SEQ ID NO:1.

Claim 2 (Original): The polynucleotide of claim 1, wherein said polynucleotide comprises at least 90% sequence identity to SEQ ID NO:1.

Claim 3 (Currently amended): [[A]]An isolated polynucleotide comprising a DNA sequence that encodes a polypeptide having at least 90% sequence identity and that retains ~~similar~~ biological activity as the unmodified sequence of SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6 and SEQ ID NO:7.

Claim 4 (Currently amended): [[A]]An isolated polynucleotide which encodes an expansin polypeptide, said polypeptide capable of restoring endogenous cell wall extension activity of heat inactivated cell walls and wherein said polynucleotide hybridizes under high stringency conditions corresponding to 6X SSC, 50% formamide and 42°C, and washing at 0.2 X SSC at 65°C with SEQ ID NO:1.

Claim 5 (Currently amended): A method of identifying a nucleotide sequence which encodes upon expression an expansin protein comprising:

obtaining an oligonucleotide of about ~~[[4]]~~8-30 contiguous bases ~~derived-obtained~~ from SEQ ID

NO:1, wherein a nucleotide sequence of said oligonucleotide is obtained by:

aligning two or more nucleotide sequences of expansins according to sequence

identity to identify a conserved sequence in said expansin sequences;

using said oligonucleotide to identify target nucleotide sequences through a hybridization, or

PCR based assay, wherein said sequences are suspected to encode a protein with expansin

activity; and thereafter

assaying the protein encoded by said target nucleotide sequence for expansin activity.

Claim 6 (Original): The method of claim 5 wherein said oligonucleotide is a PCR primer.

Claim 7 (Original): The method of claim 5 wherein said oligonucleotide is a hybridization probe.

Claim 8 (Currently amended): ~~[[A]]~~An isolated nucleotide sequence which encodes upon expression a protein with expansin activity and wherein said sequence is ~~identified-obtained~~ by the method of claim 5.

Claim 9 (Currently amended): A method of identifying a nucleotide sequence which encodes upon expression an expansin protein comprising:

obtaining an oligonucleotide fragment of about ~~[[4]]~~8-30 contiguous bases which encode

contiguous amino acids from SEQ ID NOS:2-6;

using said fragment to identify target polypeptide sequences through a hybridization or PCR based assay; and thereafter assaying a protein encoded by said polypeptide for expansin activity.

Claim 10 (Original): A polypeptide sequence identified by the method of claim 9.

Claim 11 (Currently amended): A method of identifying a nucleotide sequence which encodes upon expression an expansin protein comprising:

designing a degenerate primer to amplify expansin encoding DNA based upon SEQ ID NO:7;
amplifying a cDNA fragment from said primer;
screening a cDNA library to identify a full length coding sequence of an expansin protein.

Claim 12 (Currently amended): ~~[[A]]~~An isolated nucleotide sequence which encodes upon expression a protein with expansin activity, said sequence identified by the method of claim 11.

Claim 13 (Currently amended): A method of identifying a nucleic acid which encodes upon expression an expansin protein comprising:

obtaining an oligonucleotide of about ~~[[4]]~~8 to about 30 contiguous bases derived from SEQ ID NO:1;

using said oligonucleotide under high stringency conditions corresponding to 6X SSC, 50% formamide and 42°C, and washing at 0.2 X SSC at 65°C to identify nucleic acids that

hybridizes under stringent conditions to SEQ ID NO:1 and wherein said polynucleotide encodes a protein suspected of having expansin activity; and thereafter, assaying said protein for expansin activity.

Claim 14 (Original): The method of claim 13, wherein said oligonucleotide is a PCR primer.

Claim 15 (Original): The method of claim 13, wherein said oligonucleotide is a hybridization probe.

Claim 16 (Currently amended): A method of identifying a nucleotide sequence which encodes upon expression an expansin protein comprising:
obtaining an oligonucleotide fragment of about 8 to about 30 contiguous bases which encode contiguous amino acids from SEQ ID NOS:2-6;
using said fragments under high stringency conditions corresponding to 6X SSC, 50% formamide and 42°C, and washing at 0.2 X SSC at 65°C to identify target polypeptide sequences; and thereafter, assaying said target polypeptide sequence for expansin activity.

Claim 17 (Original): A polypeptide sequence identified by the method of claim 16.

Claim 18 (New): A method of identifying a nucleotide sequence which encodes upon expression an expansin protein comprising:

obtaining an oligonucleotide of about 8-30 contiguous bases, wherein an oligonucleotide sequence of said oligonucleotide is obtained by:

aligning two or more nucleotide sequences of expansins, wherein one of the nucleotide sequences is the nucleotide sequence of SEQ ID NO:1, according to sequence identity to identify a conserved nucleotide sequence in said expansin sequences; and

using said oligonucleotide to identify target nucleotide sequences through a hybridization or PCR based assay, wherein said sequences are suspected to encode a protein with expansin activity; and thereafter

assaying the protein encoded by said target nucleotide sequence for expansin activity.

Claim 19 (New): A method of identifying a nucleotide sequence which encodes upon expression an expansin protein comprising:

obtaining an oligonucleotide of about 8-30 contiguous bases, wherein a nucleotide sequence of said oligonucleotide is obtained by:

aligning two or more amino acid sequences of expansins, wherein one of the amino acid sequences is the amino acid sequence of SEQ ID NO:7, according to sequence identity to identify a conserved amino acid sequence in said expansin sequences; and

reverse translating said conserved amino acid sequence into a nucleotide sequence;

using said oligonucleotide to identify target nucleotide sequences through a hybridization or PCR based assay, wherein said sequences are suspected to encode a protein with expansin activity; and thereafter assaying the protein encoded by said target nucleotide sequence for expansin activity.

Claim 20 (New): A method of obtaining DNA encoding part of an expansin comprising the steps of:

obtaining an oligonucleotide of about 8-30 contiguous bases, wherein an oligonucleotide sequence of said probe is obtained by:

aligning two or more nucleotide sequences of expansins, wherein one of the nucleotide sequences is the nucleotide sequence of SEQ ID NO:1, according to sequence identity to identify a conserved nucleotide sequence in said expansin sequences; and

screening a cDNA or genomic library of an organism containing clones with said

oligonucleotide sequence in order to isolate those clones coding for an expansin containing the oligonucleotide sequence;

and obtaining clones from said library that are recognized by said oligonucleotide, so as to obtain DNA encoding part of an expansin.

Claim 21 (New): A method of obtaining DNA encoding part of an expansin, said method comprising:

selecting a DNA molecule encoding an expansin protein with expansin activity, said DNA molecule having a nucleotide sequence as shown in SEQ ID NO:1;

designing oligonucleotide primers based on aligning two or more nucleotide sequences of expansins, wherein one of the nucleotide sequences is the nucleotide sequence of SEQ ID NO:1, according to sequence identity to identify a conserved nucleotide sequence in said expansin sequences; and;

and using said oligonucleotide primers in a polymerase chain reaction (PCR) on a DNA sample to identify homologous DNA encoding an expansin protein in said sample.

Claim 22 (New): A method of obtaining DNA encoding part of an expansin, said method comprising:

selecting an expansin protein with expansin activity, said expansin having an amino acid sequence as shown in SEQ ID NO:7;

designing degenerate oligonucleotide primers based on aligning two or more nucleotide sequences of expansins, wherein one of the amino acid sequences is the amino acid sequence of SEQ ID NO:7, according to sequence identity to identify a conserved amino acid in said expansin sequences; and;

using said oligonucleotide primers in a polymerase chain reaction (PCR) on a DNA sample to identify homologous DNA encoding an expansin protein in said sample.